

Sequence Code	Sequence Name(s)	Sequence Description	Ratio	Fold Change	P-value	Sequence
YKL070W	YKL070W		46.5	46.5	0	SGD
YPL172C	COX10	Required for an essential posttranslational stage in assembly of cytochrome c oxidase	35.13	35.13	0	SGD
YKL071W	YKL071W		30.44	30.44	0	SGD
YDL243C	AAD4	high degree of similarity with the AAD of <i>P. chrysosporium</i> ; aryl-alcohol oxidase	29.17	29.17	0	SGD
YBR244W	GPX2,AMI1	Glutathione peroxidase parologue; Null mutant is viable	14.16	14.16	0	SGD
YLR460C	YLR460C		13.98	13.98	0	SGD
YKR065C	YKR065C		12.93	12.93	0	SGD
YOR224C	RPB8	16-kDa RNA polymerase subunit (common to polymerases I, II and III)	11.01	11.01	0	SGD
YOL151W	GRE2	induced by osmotic stress, similar to dihydroflavonol 4-reductase family	10.72	10.72	0	SGD
YLR077W	YLR077W		10.09	10.09	0	SGD
YKR077W	YKR077W		9.98	9.98	7.82E-40	SGD
YML131W	YML131W		9.76	9.76	0	SGD
YBR008C	FLR1	Fluconazole Resistance 1; major facilitator transporter; Null mutant is viable	9.37	9.37	0	SGD
YNL176C	YNL176C		9.35	9.35	0	SGD
YEL053C	MAK10	Glucose-repressible protein; Null mutant is viable, grows poorly or not at all	9.04	9.04	2.48E-32	SGD
YIL167W	YIL167W		9.01	9.01	0	SGD
YOL157C	YOL157C		8.86	8.86	0	SGD
YJL221C	FSP2	homology to maltase(alpha-D-glucosidase); similar to maltase (alpha-D-glucosidase)	8.85	8.85	0	SGD
YIL172C	YIL172C	putative alpha glucosidase	8.82	8.82	0	SGD
YOL150C	YOL150C		8.52	8.52	6.41E-26	SGD
YJR156C	THI11	thiamine regulated gene, homologous to <i>S. pombe</i> NMT1A. Proposed function: L-serine dehydratase	7.19	7.19	0	SGD
YIL168W	SDL1		7.15	7.15	1.22E-22	SGD
YGR209C	TRX2	thioredoxin; Null mutant is viable, trx1-trx2 double mutant shows partial growth defect	6.82	6.82	0	SGD
YDR355C	YDR355C		6.8	6.8	1.21E-39	SGD
YFL056C	AAD6	high degree of similarity with the AAD of <i>P. chrysosporium</i> ; aryl-alcohol oxidase	6.74	6.74	0	SGD
YDL244W	THI13	Product of gene unknown	6.5	6.5	0	SGD
YHR180W	YHR180W		6.33	6.33	0	SGD
YDR353W	TRR1	Thioredoxin reductase; thioredoxin reductase; Null mutant is viable	6.09	6.09	8.00E-41	SGD
YDL242W	YDL242W		5.64	5.64	8.67E-31	SGD
YOR226C	ISU2,NUA2	Iron-sulfur cluster nifU-like protein; Null mutant is viable on YPD and SD medium	5.62	5.62	1.22E-39	SGD
YPR200C	ARR2	Required for arsenate but not for arsenite resistance; Null mutant is viable	5.61	5.61	0	SGD
YDR132C	YDR132C		5.58	5.58	0	SGD
YJL219W	HXT9	High-affinity hexose transporter; hexose permease; Null mutant is viable	5.56	5.56	0	SGD
YNL332W	THI12	thiamine regulated gene, homologous to nmt1a in <i>Schizosaccharomyces pombe</i>	5.42	5.42	0	SGD
YBL067C	UBP13	similar to Ubp9p; ubiquitin carboxyl-terminal hydrolase	5.19	5.19	0	SGD
YML091C	RPM2	involved in processing of mitochondrial precursor tRNAs and proteins	5.05	5.05	1.36E-27	SGD

YFL058W	THI5	proposed biosynthetic enzyme involved in pyrimidine biosynthesis	5.01	5.01	0 SGD
YDL168W	SFA1	Long-chain alcohol dehydrogenase (glutathione-dependent formal	4.86	4.86	0 SGD
YGR208W	SER2	phosphoserine phosphatase; serine-requiring	4.75	4.75	4.92E-16 SGD
YML007W	YAP1,PAR1,SNQ3	jun-like transcription factor; pleiotropic drug resistance	4.72	4.72	5.61E-45 SGD
YLR108C	YLR108C		4.66	4.66	0 SGD
YCL026C-A	FRM2	Protein involved in the integration of lipid signaling pathways with	4.55	4.55	0 SGD
YLL056C	YLL056C		4.45	4.45	0 SGD
YJL220W	YJL220W		4.4	4.4	5.13E-15 SGD
YNL212W	VID27	Vacuole import and degradation; Null mutant is viable but exhibits	4.28	4.28	0 SGD
YCR102C	YCR102C		4.26	4.26	3.67E-11 SGD
YLL060C	GTT2	Glutathione Transferase; glutathione transferase; Null mutant is vi	4	4	8.58E-30 SGD
YOL156W	HXT11,LGT3	High-affinity hexose transporter; glucose permease; Null mutant is	3.86	3.86	4.97E-12 SGD
YDR354W	TRP4	anthranilate phosphoribosyl transferase; tryptophan requiring	3.69	3.69	0 SGD
YJR122W	CAF17	CCR4 associated factor; CCR4 transcriptional complex compone	3.58	3.58	1.16E-35 SGD
YLR076C	YLR076C		3.57	3.57	1.47E-29 SGD
YDL218W	YDL218W		3.56	3.56	2.21E-21 SGD
YML087C	YML087C		3.55	3.55	0 SGD
YIR030C	DCG1	Product of gene unknown	3.54	3.54	5.12E-22 SGD
YCR105W	YCR105W	Alcohol dehydrogenase	3.53	3.53	0 SGD
YDL241W	YDL241W		3.52	3.52	1.06E-09 SGD
YER148W	SPT15,BTF1,TBP1,TFIID	TATA-binding protein (tfIID); TFIID subunit; Null mutant is inviable	3.5	3.5	8.52E-33 SGD
YML028W	TSA1,TPX1,ZRG14	antioxidant enzyme that provides protection against oxidation syst	3.46	3.46	2.47E-40 SGD
YKL043W	PHD1	protein similar to StuA of <i>Aspergillus nidulans</i> ; transcription factor	3.42	3.42	0 SGD
YMR318C	YMR318C		3.37	3.37	3.10E-14 SGD
YNR074C	YNR074C		3.37	3.37	0 SGD
YJR048W	CYC1	iso-1-cytochrome c; Cytochrome c deficiency	3.36	3.36	3.10E-31 SGD
YGR223C	YGR223C		3.33	3.33	6.66E-41 SGD
YPR048W	TAH18	Product of gene unknown; tah18-1 mutant is hypersensitive to hyc	3.3	3.3	0 SGD
YFR039C	YFR039C		3.28	3.28	2.14E-24 SGD
YPL173W	MRPL40	Mitochondrial ribosomal protein MRPL40 (YmL40); ribosomal prot	3.27	3.27	0 SGD
YNL135C	FPR1,FKB1,RBP1	FK506 binding protein, proline rotamase, rapamycin-binding prote	3.18	3.18	1.54E-14 SGD
YDR368W	YPR1	homologous to the aldo-keto reductase protein family	3.16	3.16	0 SGD
YGL091C	NBP35	NBP35 encodes an essential evolutionary conserved protein with	3.12	3.12	1.62E-06 SGD
YOR058C	ASE1	essential for anaphase spindle elongation; spindle midzone compo	3.11	3.11	0 SGD
YMR037C	MSN2	multiplicity suppressor of snf1 mutation; zinc finger protein; Null mu	3.1	3.1	1.58E-21 SGD
YIL171W	HXT12	High level of sequence similarity to HXT1 and HXT9 hexose trans	3.06	3.06	0 SGD
YGR234W	YHB1,YHB4	may play a role in the oxidative stress response; flavohemoglobin;	3.05	3.05	0 SGD

YKR067W	GPT2	Encodes a Glycerol-3-phosphate acyltransferase; Null: viable.	3.04	3.04	1.66E-33 SGD
YOR152C	YOR152C		3.03	3.03	7.81E-14 SGD
YLR457C	NBP1	Nap1p Binding Protein; Null mutant is inviable	2.98	2.98	2.09E-16 SGD
YHR198C	YHR198C		2.97	2.97	0 SGD
YLR113W	HOG1,SSK3	osmoregulation; MAP kinase; Null mutant is viable and unable to c	2.94	2.94	1.90E-22 SGD
YDR131C	YDR131C		2.91	2.91	2.36E-11 SGD
YJL058C	YJL058C		2.91	2.91	1.88E-13 SGD
YKL085W	MDH1	mitochondrial malate dehydrogenase; malate dehydrogenase; Nul	2.89	2.89	3.69E-41 SGD
YIL170W	HXT12	High level of sequence similarity to HXT1 and HXT9 hexose trans	2.84	2.84	0 SGD
YPL202C	AFT2	Activator of Iron (Fe) Transcription; Null: Deletion of AFT2 exacerbates overexpression Rescues sro7/sop1 in NaCl; viable in both high an	2.83	2.83	1.09E-14 SGD
YMR266W	RSN1		2.81	2.81	1.67E-19 SGD
YMR172C-A	YMR172C-A		2.8	2.8	4.05E-15 SGD
YOL124C	YOL124C		2.8	2.8	1.39E-12 SGD
YPR094W	YPR094W		2.79	2.79	0 SGD
YCL029C	BIK1,ARM5,PAC14	Microtubule-associated protein required for microtubule function d	2.77	2.77	5.48E-11 SGD
YKL087C	CYT2	links heme covalently to apocytochrome c1; cytochrome c1 heme	2.77	2.77	1.37E-09 SGD
YMR175W	SIP18	Salt-Induced Protein; Null mutant is viable.	2.76	2.76	7.89E-23 SGD
YLL054C	YLL054C		2.75	2.75	0 SGD
YLR163C	MAS1,MIF1	mitochondrial processing protease subunit; Null mutant is inviable	2.72	2.72	0 SGD
YKL107W	YKL107W		2.7	2.7	0 SGD
YLR075W	RPL10,GRC5,QSR1	similar to members of the QM gene family, which is implicated in c	2.7	2.7	3.44E-13 SGD
YML077W	BET5	Bet5p/18kD component of TRAPP; TRAPP 18kDa component; Nu	2.69	2.69	3.26E-12 SGD
YOL116W	MSN1,FUP1,HRB382,MSS1	(multicopy suppressor of snf1 and sta10 mutations; 43 kDa protein,	2.62	2.62	6.98E-13 SGD
YGR224W	AZR1	MFS-MDR	2.58	2.58	2.07E-09 SGD
YML116W	ATR1,SNQ1	aminotriazole resistance; very hydrophobic, has many membrane-	2.57	2.57	5.62E-14 SGD
YKL042W	SPC42	involved in SPB duplication, may facilitate attachment of the SPB	2.55	2.55	1.02E-27 SGD
YKL069W	YKL069W		2.55	2.55	0 SGD
YER143W	DDI1,VSM1	DNA Damage Inducible, binds to T- and V- snare complexes; Null	2.53	2.53	2.78E-37 SGD
YJL103C	YJL103C		2.53	2.53	0 SGD
YKL083W	YKL083W		2.52	2.52	5.02E-18 SGD
YGR249W	MGA1	Mga1p shows similarity to heat shock transcription factor; similar t	2.51	2.51	1.91E-23 SGD
YNR062C	YNR062C		2.51	2.51	3.98E-07 SGD
YBR243C	ALG7,TUR1	ER protein that transfers Glc-Nac-P from UDP-GlcNac to Dol-P; U	2.49	2.49	3.18E-43 SGD
YGL252C	RTG2	Protein involved in interorganelle communication between mitochondria	2.49	2.49	1.97E-08 SGD
YLR312W-A	MRPL15	Mitochondrial ribosomal protein MRPL15 (YmL15); ribosomal prot	2.48	2.48	7.97E-16 SGD
YPR065W	ROX1,REO1	The ROX1 gene encodes a heme-induced repressor of hypoxic gene	2.46	2.46	2.75E-09 SGD
YKL223W	YKL223W		2.45	2.45	9.02E-25 SGD

YIL142W	CCT2,BIN3,TCP2	cytoplasmic chaperonin of the Cct ring complex related to Tcp1p, involved in protein folding	2.44	2.44	1.29E-07	SGD
YKL044W	YKL044W		2.44	2.44	8.78E-14	SGD
YGL260W	YGL260W		2.4	2.4	2.59E-30	SGD
YNR066C	YNR066C		2.4	2.4	0	SGD
YIL108W	YIL108W		2.39	2.39	4.56E-18	SGD
YCR102W-A	ORF:YCR102W-A	BioProcess=biological_process unknown MolFunction=molecular_function	2.37	2.37	0	SGD
YIL174W	YIL174W		2.37	2.37	1.41E-26	SGD
YLR458W	YLR458W		2.37	2.37	1.30E-30	SGD
YNL211C	YNL211C		2.35	2.35	3.37E-11	SGD
YDL167C	NRP1	asparagine-rich protein	2.34	2.34	6.45E-22	SGD
YJL218W	YJL218W		2.34	2.34	5.21E-22	SGD
YPL091W	GLR1,LPG17	converts oxidized glutathione and NADPH into two glutathiones and NADH	2.33	2.33	1.02E-26	SGD
YDL202W	MRPL11	Mitochondrial ribosomal protein MRPL11 (YmL11); ribosomal protein L11	2.31	2.31	1.07E-13	SGD
YOL148C	SPT20,ADA5	Transcription factor; histone acetyltransferase SAGA complex member	2.31	2.31	0	SGD
YDR227W	SIR4,ASD1,STE9,UTH2	regulator of silencing at HML, HMR, and telomeres; silencing regulator	2.29	2.29	7.14E-06	SGD
YKL093W	MBR1	Involved in mitochondrial biogenesis; Null mutant is viable, shows growth defect	2.29	2.29	2.63E-16	SGD
YFL055W	AGP3	General amino acid permease with broad substrate specificity; amylase permease	2.28	2.28	1.68E-13	SGD
Q0070	AI5_ALPHA	Intron of mitochondrial COX1, al5-alpha; DNA endonuclease involved in DNA repair	2.24	2.24	7.42E-04	SGD
YDR036C	YDR036C		2.23	2.23	2.32E-20	SGD
YOL115W	TRF4	TRF5 homolog, Involved in mitotic chromosome condensation, associated with centromeres	2.22	2.22	1.45E-11	SGD
YHR184W	SSP1,SPO3	Involved in the control of meiotic nuclear divisions & spore formation	2.21	2.21	5.50E-05	SGD
YML041C	YML041C		2.2	2.2	1.74E-11	SGD
YNL174W	YNL174W		2.2	2.2	2.87E-28	SGD
YPR201W	ARR3	Putative membrane protein involved in arsenite transport; Overexpressed in yeast	2.2	2.2	4.94E-09	SGD
YJL097W	YJL097W		2.18	2.18	1.31E-32	SGD
YEL052W	AFG1	ATPase family gene; ATPase family	2.16	2.16	6.11E-33	SGD
YIR040C	YIR040C		2.16	2.16	2.31E-32	SGD
YKR105C	YKR105C		2.16	2.16	1.36E-04	SGD
YNL012W	SPO1	dispensable for mitosis, premeiotic DNA synthesis, synaptonemal	2.14	2.14	8.71E-26	SGD
YJR157W	YJR157W		2.13	2.13	3.54E-35	SGD
YNL207W	YNL207W		2.11	2.11	8.39E-33	SGD
YFL063W	YFL063W		2.1	2.1	4.22E-20	SGD
YCL027W	FUS1	cell-surface protein required for cell fusion; Null mutant is viable, irregular growth	2.08	2.08	4.53E-06	SGD
YKR066C	CCP1	Cytochrome-c peroxidase; cytochrome c peroxidase	2.08	2.08	3.24E-28	SGD
YMR169C	ALD3	Expression induced in response to heat shock, oxidative and osmotic stress	2.08	2.08	9.88E-13	SGD
YJL031C	BET4	catalyzes prenylation of Ypt1p (as a subunit of PGGTase-II); general	2.07	2.07	5.00E-28	SGD
YMR301C	ATM1	mitochondrial ABC transporter protein; ABC transporter; slow growth	2.07	2.07	5.13E-08	SGD

YJR023C	YJR023C		2.04	2.04	7.13E-05 SGD
YNL185C	MRPL19	mitochondrial ribosomal protein of the large subunit; ribosomal prc	2.04	2.04	5.98E-20 SGD
YDR003W	YDR003W		2.03	2.03	1.48E-09 SGD
YDR278C	YDR278C		2.03	2.03	7.73E-10 SGD
YDR485C	YDR485C		2.03	2.03	1.32E-15 SGD
YGR172C	YIP1	Golgi integral membrane protein, binds to the transport GTPases involved in regulated secretion/recycling of nitrogen regulated peri	0.5	-2	6.57E-08 SGD
YKL176C	LST4	Protein involved in RNA processing and export from nucleus; GTF	0.5	-2.01	3.65E-12 SGD
YMR235C	RNA1	RUVB-like protein, TIP49b Homologue; transcriptional regulator; N	0.5	-2.01	2.24E-13 SGD
YPL235W	RVB2,TIH2,TIP49B	vacuolar ATPase V1 domain subunit H (54 kDa); vacuolar H(+) A _T	0.49	-2.02	1.95E-25 SGD
YFR044C	YFR044C	oxidizes ubiquinol at center P in the protonmotive Q cycle mechan	0.49	-2.03	6.28E-06 SGD
YPR036W	VMA13,CLS11	Required for entry into stationary phase, heat shock-resistance, a	0.49	-2.03	7.55E-06 SGD
YEL024W	RIP1	alpha subunit of pyruvate dehydrogenase (E1 alpha); pyruvate de	0.49	-2.04	3.56E-43 SGD
YDL040C	NAT1,AAA1		0.49	-2.05	3.85E-06 SGD
YER178W	PDA1		0.49	-2.05	1.16E-21 SGD
YMR247C	YMR247C		0.49	-2.05	0 SGD
YNL097C	PHO23	Involved in expression of PHO5; Null mutant is viable but shows c	0.49	-2.05	2.26E-13 SGD
YBR105C	VID24	also involved in vacuolar protein targeting; peripheral vesicle mem	0.48	-2.07	2.95E-36 SGD
YKL023W	YKL023W		0.48	-2.08	3.64E-16 SGD
YMR020W	FMS1	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), :	0.48	-2.08	1.22E-09 SGD
YNL032W	SIW14	Synthetic interaction with Whi2; tyrosine phosphatase; Null mutant	0.48	-2.08	2.38E-08 SGD
YBR221C	PDB1	beta subunit of pyruvate dehydrogenase (E1 beta); pyruvatedehy	0.48	-2.09	1.72E-16 SGD
YNL294C	RIM21,PAL3	Regulator of IME2; Unknown function; Null: Affected in sporulatio	0.48	-2.09	3.67E-14 SGD
YNL310C	YNL310C		0.48	-2.09	2.21E-10 SGD
YCR044C	PER1	Protein Processing in the ER	0.48	-2.1	3.12E-08 SGD
YFL027C	GYP8	GAP for Ypt protein; GTPase-activating protein; Null: viable	0.48	-2.1	7.92E-18 SGD
YKR027W	YKR027W		0.48	-2.1	7.84E-13 SGD
YJR127C	ZMS1	Product of gene unknown	0.47	-2.11	2.61E-04 SGD
YDR483W	KRE2,MNT1	N-glycosylation; alpha-1,2-mannosyltransferase; have altered N-li	0.47	-2.12	1.15E-25 SGD
YIL091C	YIL091C		0.47	-2.12	3.41E-11 SGD
YKL077W	YKL077W		0.47	-2.12	2.05E-26 SGD
YNL280C	ERG24	sterol C-14 reductase; Null mutant appears to be inviable in some	0.47	-2.12	0 SGD
YDL215C	GDH2	NAD-dependent glutamate dehydrogenase; Null mutant is viable,	0.47	-2.13	0 SGD
YGL140C	YGL140C		0.47	-2.13	3.11E-11 SGD
YNL227C	YNL227C		0.47	-2.13	1.60E-24 SGD
YNL169C	PSD1	converts phosphatidylserine to phosphatidylethanolamine; phosph	0.47	-2.14	1.31E-09 SGD
YOR251C	YOR251C		0.46	-2.15	3.78E-13 SGD
YGL196W	YGL196W		0.46	-2.17	1.23E-27 SGD

YHR072W	ERG7	carries out complex cyclization step of squalene to lanosterol in st	0.46	-2.17	1.97E-28 SGD
YLR371W	ROM2	Gdp-GTP Exchange Protein (GEP) for the Rho1p Small GTP-bind	0.46	-2.17	3.23E-10 SGD
YOL130W	ALR1	aluminium resistance; ion transporter (putative); Null mutant is inv	0.46	-2.17	2.77E-09 SGD
YPL145C	KES1,LPI3,OSH4	Homologous to human oxysterol-binding protein, implicated in erg	0.46	-2.17	3.00E-31 SGD
YPL087W	YDC1	Yeast dihydro-ceramidase; alkaline dihydroceramidase with minor	0.46	-2.18	6.07E-05 SGD
YGL206C	CHC1,SWA5	presumed vesicle coat protein; Clathrin heavy chain; Null mutant i	0.46	-2.19	8.42E-21 SGD
YLR179C	YLR179C		0.46	-2.19	1.02E-11 SGD
YNL168C	YNL168C		0.46	-2.2	0 SGD
YOR292C	YOR292C		0.45	-2.2	6.80E-23 SGD
YDR119W	YDR119W		0.45	-2.21	2.71E-10 SGD
YPR058W	YMC1	putative mitochondrial carrier protein; carrier protein (putative)	0.45	-2.21	1.07E-39 SGD
YAL044W-A	ORF:YAL044W-A	BioProcess=biological_process unknown MolFunction=molecular_	0.45	-2.22	3.25E-43 SGD
YLR358C	YLR358C		0.45	-2.23	1.26E-10 SGD
YMR029C	YMR029C		0.45	-2.23	1.18E-28 SGD
YMR153W	NUP53	Component of karyopherin docking complex of the nuclear pore co	0.45	-2.23	0 SGD
YCR097W	HMRA1,A1,MATA1	silenced copy of A1, which encodes a homeobox-domain containin	0.45	-2.24	2.26E-05 SGD
YER033C	ZRG8	Zinc regulated gene	0.44	-2.26	7.68E-28 SGD
YOR122C	PFY1,PRF1	profilin (actin-binding protein); profilin; Null mutant is either inviable	0.44	-2.26	1.08E-06 SGD
YLL032C	YLL032C		0.44	-2.27	1.74E-23 SGD
YOR241W	MET7	METHionine requiring; folylpolyglutamate synthetase; Null mutant	0.44	-2.27	1.47E-27 SGD
YPL268W	PLC1	Hydrolyzes phosphatidylinositol 4,5-biphosphate (PIP2) to genera	0.44	-2.27	1.71E-15 SGD
YER062C	HOR2,GPP2	RHR2 (GPP1) encodes another DL-glycerol-3-phosphatase; DL-g	0.44	-2.28	1.71E-36 SGD
YER119C	YER119C	similar to amino acid transport proteins	0.44	-2.28	4.24E-17 SGD
YOR323C	PRO2	gamma-glutamyl phosphate reductase; Proline requiring and unab	0.44	-2.28	8.53E-42 SGD
YEL071W	DLD3	D-lactate dehydrogenase	0.44	-2.29	9.75E-09 SGD
YBR145W	ADH5	alcohol dehydrogenase isoenzyme V	0.43	-2.31	1.02E-04 SGD
YER155C	BEM2,IPL2,SUP9,TSL1	Protein with role in bud emergence; rho GTPase activating protein	0.43	-2.31	1.95E-17 SGD
YLR189C	UGT51	Udp-glycosyltransferase; UDP-glucose:sterol glucosyltransferase;	0.43	-2.31	1.29E-33 SGD
YOR298C-A	MBF1	bridges the DNA-binding region of GCN4 and TBP, similar to mult	0.43	-2.31	2.82E-34 SGD
YPR074C	TKL1	Transketolase 1; transketolase 1; Null mutant is viable, growth on	0.43	-2.31	3.17E-20 SGD
YBR183W	YPC1	Yeast Phyto-ceramidase; alkaline ceramidase with reverse activity	0.43	-2.32	4.55E-24 SGD
YDL112W	TRM3	Trna ribose methylase; tRNA (Gm18) ribose methylase; Null muta	0.43	-2.32	9.62E-13 SGD
YHR001W-A	QCR10	8.5 kDa subunit of the ubiquinol-cytochrome c oxidoreductase corr	0.43	-2.32	7.09E-07 SGD
YGR170W	PSD2	converts phosphatidylserine to phosphatidylethanolamine; phosph	0.43	-2.33	5.60E-11 SGD
YGR191W	HIP1	histidine permease; requires supplementation with large amounts	0.43	-2.33	0 SGD
YLR241W	YLR241W		0.43	-2.33	5.47E-42 SGD
YOR273C	TPO4	Polyamine transport protein	0.43	-2.34	3.97E-34 SGD

YER080W	YER080W		0.43	-2.35	2.11E-10	SGD
YHR208W	BAT1,ECA39,TWT1	branched-chain amino acid transaminase, highly similar to mammal	0.43	-2.35	7.43E-38	SGD
YOR288C	MPD1	Disulfide isomerase related protein; disulfide isomerase related protein	0.43	-2.35	5.23E-07	SGD
YPL128C	TBF1,LPI16	TTAGGG repeat binding factor; lethal	0.43	-2.35	1.14E-13	SGD
YDR298C	ATP5,OSC1	Subunit 5 of the mitochondrial ATP synthase complex, homologous to	0.42	-2.36	0	SGD
YDR474C	YDR474C		0.42	-2.36	8.80E-32	SGD
YML035C	AMD1,AMD3	putative alpha-mannosidase; alpha-mannosidase (putative); Null mutant is viable.	0.42	-2.36	0	SGD
YMR271C	URA10	Fifth step in pyrimidine bio5; orotate phosphoribosyltransferase 2; S-adenosylmethionine synthetase; Null mutant is viable.	0.42	-2.36	8.78E-09	SGD
YLR180W	SAM1,ETH10	123 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase	0.42	-2.37	2.25E-06	SGD
YML100W	TSL1		0.42	-2.37	2.66E-05	SGD
YLR285W	YLR285W		0.42	-2.38	1.54E-07	SGD
YPR191W	QCR2,COR2,UCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2; Null mutant is viable.	0.42	-2.38	2.05E-16	SGD
YLR425W	TUS1,SOP10	TOR Unique function Suppressor, exchange factor for RHO1; 130 kDa	0.42	-2.4	0	SGD
YNL268W	LYP1	lysine permease	0.42	-2.4	2.80E-25	SGD
YPL094C	SEC62,LPG14	membrane component of ER protein translocation apparatus; ER membrane protein	0.42	-2.4	3.63E-38	SGD
YPL022W	RAD1,LPB9	UV endonuclease; radiation sensitive	0.42	-2.41	8.36E-09	SGD
YBR263W	SHM1,SHMT1,TMP3	Serine hydroxymethyltransferase, mitochondrial; Null mutant is viable.	0.41	-2.42	0	SGD
YER175C	TMT1,TAM1	Trans-aconitate Methyltransferase 1	0.41	-2.44	2.27E-04	SGD
YKL060C	FBA1	aldolase; Null mutant is viable, lacks aldolase enzymatic activity and viability	0.41	-2.44	6.69E-24	SGD
YOL086C	ADH1,ADC1	Alcohol dehydrogenase; alcohol dehydrogenase; Null mutant is viable.	0.41	-2.45	1.23E-23	SGD
YKR096W	YKR096W		0.41	-2.47	4.38E-34	SGD
YNL138W	SRV2,CAP	70-kDa adenylyl cyclase-associated protein; 70 kDa adenylyl cyclase-associated protein	0.41	-2.47	1.23E-04	SGD
YMR221C	YMR221C		0.4	-2.49	3.77E-04	SGD
YGR261C	APL6,YKS5	beta3-like subunit of the yeast AP-3 complex which functions in transport	0.4	-2.5	1.96E-40	SGD
YLR355C	ILV5	branched-chain amino acid biosynthesis; acetohydroxyacid reductotransformase	0.4	-2.5	7.06E-23	SGD
YOR184W	SER1,ADE9	phosphoserine transaminase; Null mutant is viable, serine-requiring	0.4	-2.5	1.37E-17	SGD
YPR114W	YPR114W		0.4	-2.5	8.78E-12	SGD
YMR319C	FET4	Putative transmembrane low-affinity Fe(II) transporter; low affinity iron transporter	0.4	-2.53	1.91E-28	SGD
YAL038W	CDC19,PYK1	Required for START A in the cell cycle and sporulation; pyruvate kinase	0.39	-2.54	6.41E-04	SGD
YMR219W	ESC1	Establishes Silent Chromatin	0.39	-2.54	3.91E-36	SGD
YCL030C	HIS4	histidinol dehydrogenase; Null mutant is viable and requires histidine	0.39	-2.56	5.37E-34	SGD
YCR073W-A	SOL2	multicopy suppressor of los1-1; Null mutant is viable	0.39	-2.56	0	SGD
YMR237W	YMR237W		0.39	-2.56	3.96E-20	SGD
YGR127W	YGR127W		0.39	-2.58	1.12E-17	SGD
YNL104C	LEU4	leucine biosynthesis; alpha-isopropylmalate synthase (2-isopropylmalate synthase)	0.39	-2.59	0	SGD
YMR196W	YMR196W		0.38	-2.61	0	SGD
YCL009C	ILV6	acetolactate synthase regulatory subunit	0.38	-2.62	1.27E-04	SGD

YPL084W	BRO1,LPF2	BCK1-like resistance to osmotic shock; Temperature-sensitive grc	0.38	-2.64	1.86E-12	SGD
YDR154C	YDR154C		0.38	-2.65	5.89E-04	SGD
YDL237W	YDL237W		0.37	-2.67	1.16E-39	SGD
YER061C	CEM1	homology with beta-keto-acyl synthases; beta-keto-acyl synthase	0.37	-2.67	7.67E-09	SGD
YDL022W	GPD1,DAR1,HOR1,OSG1,O	glycerol-3-phosphate dehydrogenase; lethal under conditions of o	0.37	-2.7	0	SGD
YOR136W	IDH2	NAD+-dependent isocitrate dehydrogenase; NAD-dependent isoc	0.37	-2.72	4.54E-10	SGD
YBL015W	ACH1	Mannose-containing glycoprotein which binds concanavalin A; acce	0.37	-2.74	0	SGD
YPL262W	FUM1	Fumarase converts l-malate to fumarate as part of the TCA cycle;	0.35	-2.82	0	SGD
YJL134W	LCB3,LBP1,YSR2	Protein involved in incorporation of exogenous long chain bases ir	0.35	-2.85	7.78E-20	SGD
YHR087W	YHR087W		0.35	-2.86	1.37E-23	SGD
YLR354C	TAL1	Transaldolase, enzyme in the pentose phosphate pathway; transa	0.35	-2.89	0	SGD
YDL155W	CLB3	Involved in mitotic induction and perhaps in DNA replication and s	0.33	-3.04	6.42E-17	SGD
YKL151C	YKL151C		0.32	-3.15	2.80E-45	SGD
YMR297W	PRC1,LBC1	dispensable for haploidization and sporulation, but required for full	0.32	-3.17	0	SGD
YMR203W	TOM40,ISP42,MOM38	Translocase of Outer Mitochondrial membrane; forms the outer m	0.31	-3.18	0	SGD
YDL048C	STP4	Involved in pre-tRNA splicing and in uptake of branched-chain am	0.3	-3.32	4.19E-23	SGD
YKL029C	MAE1	Mitochondrial malic enzyme; malic enzyme; null mutant exhibits no	0.27	-3.76	1.58E-32	SGD

Sequence ID

639074 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637915 BioProcess=heme a biosynthesis|MolFunction=protoheme IX farnesyltransferase|CellComponent=mitochondrial inner membrane
634516 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636642 BioProcess=aldehyde metabolism|MolFunction=benzyl alcohol dehydrogenase|CellComponent=cellular_component unknown
634399 BioProcess=not yet annotated|MolFunction=glutathione peroxidase|CellComponent=not yet annotated
638533 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637602 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634943 BioProcess=transcription from Pol II promoter*|MolFunction=DNA-directed RNA polymerase III*|CellComponent=DNA-directed RNA polymerase III c
633862 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636242 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636028 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636011 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639463 BioProcess=not yet annotated|MolFunction=transporter|CellComponent=not yet annotated
636916 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634135 BioProcess=N-terminal protein amino acid acetylation*|MolFunction=amino acid N-acetyltransferase|CellComponent=cellular_component unknown
634972 BioProcess=gluconeogenesis|MolFunction=not yet annotated|CellComponent=not yet annotated
638005 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
637989 BioProcess=not yet annotated|MolFunction=alpha-glucosidase|CellComponent=not yet annotated
639489 BioProcess=not yet annotated|MolFunction=alpha-glucosidase|CellComponent=not yet annotated
634857 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639311 BioProcess=thiamin biosynthesis|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
639098 BioProcess=not yet annotated|MolFunction=L-serine ammonia-lyase|CellComponent=not yet annotated
638175 BioProcess=response to oxidative stress*|MolFunction=thiol-disulfide exchange intermediate|CellComponent=cytosol*
634880 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638319 BioProcess=aldehyde metabolism|MolFunction=benzyl alcohol dehydrogenase|CellComponent=cellular_component unknown
633863 BioProcess=thiamin biosynthesis|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
634415 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635131 BioProcess=regulation of redox homeostasis|MolFunction=thioredoxin reductase (NADPH)|CellComponent=not yet annotated
635761 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638278 BioProcess=iron homeostasis|MolFunction=molecular_function unknown|CellComponent=mitochondrial matrix
637485 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638574 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634112 BioProcess=hexose transport|MolFunction=glucose transporter*|CellComponent=not yet annotated
635939 BioProcess=thiamin biosynthesis|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
635409 BioProcess=deubiquitination|MolFunction=ubiquitin-specific protease|CellComponent=cellular_component unknown
637400 BioProcess=protein biosynthesis*|MolFunction=ribonuclease P|CellComponent=mitochondrion

633843 BioProcess=thiamin biosynthesis|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
638525 BioProcess=not yet annotated|MolFunction=acyl/glycerone-phosphate reductase|CellComponent=not yet annotated
634544 BioProcess=not yet annotated|MolFunction=phosphoserine phosphatase|CellComponent=not yet annotated
634566 BioProcess=response to oxidative stress*|MolFunction=not yet annotated|CellComponent=cytoplasm*
638596 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637621 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635150 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634320 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636260 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639273 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635099 BioProcess=glutathione metabolism|MolFunction=glutathione transferase|CellComponent=not yet annotated
636191 BioProcess=hexose transport|MolFunction=glucose transporter*|CellComponent=not yet annotated
635173 BioProcess=tryptophan biosynthesis|MolFunction=anthranilate phosphoribosyltransferase|CellComponent=not yet annotated
635286 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
634253 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634535 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm
636673 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637682 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
639279 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637493 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639161 BioProcess=transcription initiation from Pol II promoter*|MolFunction=DNA binding*|CellComponent=nucleus*
633736 BioProcess=response to oxidative stress*|MolFunction=thioredoxin peroxidase|CellComponent=cytoplasm
637779 BioProcess=pseudohyphal growth|MolFunction=specific RNA polymerase II transcription factor|CellComponent=nucleus
639280 BioProcess=aldehyde metabolism*|MolFunction=alcohol dehydrogenase (NADP+)|CellComponent=soluble fraction
635237 BioProcess=response to singlet oxygen|MolFunction=not yet annotated|CellComponent=plasma membrane
634295 BioProcess=oxidative phosphorylation|MolFunction=not yet annotated|CellComponent=not yet annotated
633942 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636911 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635345 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634554 BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit
633543 BioProcess=biological_process unknown|MolFunction=peptidyl-prolyl cis-trans isomerase|CellComponent=cytoplasm
635121 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636957 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637297 BioProcess=mitotic anaphase B*|MolFunction=microtubule binding|CellComponent=spindle microtubule*
638038 BioProcess=stress response*|MolFunction=not yet annotated|CellComponent=not yet annotated
638166 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
635207 BioProcess=stress response|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown

633406 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm*
635105 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634518 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
636715 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637884 BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=cytoplasm
636213 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636204 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639300 BioProcess=tricarboxylic acid cycle*|MolFunction=malic enzyme|CellComponent=mitochondrial matrix
636160 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
638547 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637315 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635745 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636047 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638154 BioProcess=response to xenobiotic|MolFunction=transcription factor|CellComponent=cellular_component unknown
633931 BioProcess=mitotic anaphase B*|MolFunction=microtubule binding|CellComponent=spindle pole body*
636583 BioProcess=cytochrome c-heme linkage|MolFunction=holocytochrome c synthase|CellComponent=mitochondrion
633396 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
634753 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636105 BioProcess=mitochondrial processing|MolFunction=beta-mitochondrial processing peptidase|CellComponent=mitochondrial matrix
635158 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638296 BioProcess=protein biosynthesis*|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)
636467 BioProcess=ER to Golgi transport|MolFunction=molecular_function unknown|CellComponent=TRAPP
635172 BioProcess=hyperosmotic response|MolFunction=molecular_function unknown|CellComponent=nucleus
636921 BioProcess=transport|MolFunction=transporter|CellComponent=membrane
639466 BioProcess=multidrug transport|MolFunction=multidrug efflux pump|CellComponent=plasma membrane
633880 BioProcess=microtubule nucleation*|MolFunction=structural constituent of cytoskeleton|CellComponent=central plaque of spindle pole body*
635799 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637826 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637145 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
633286 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634040 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638430 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637875 BioProcess=N-linked glycosylation|MolFunction=UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosamine-1-phosphate transferase|CellCc
634101 BioProcess=intracellular signaling cascade|MolFunction=molecular_function unknown|CellComponent=cytoplasm
633350 BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit
639342 BioProcess=negative regulation of transcription from Pol II promoter|MolFunction=DNA bending*|CellComponent=nuclear chromosome
638148 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

637157 BioProcess=protein folding*|MolFunction=chaperone|CellComponent=cytoplasm*

636325 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634788 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

633950 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634709 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

970817 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638103 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

633629 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634218 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638049 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown

637619 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638638 BioProcess=not yet annotated|MolFunction=glutathione reductase (NADPH)|CellComponent=not yet annotated

633716 BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit

637195 BioProcess=chromatin modification*|MolFunction=not yet annotated|CellComponent=SAGA complex

638953 BioProcess=chromatin silencing at telomere*|MolFunction=not yet annotated|CellComponent=nucleolus*

633802 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated

637985 BioProcess=transport|MolFunction=general amino acid permease|CellComponent=not yet annotated

970792 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

637092 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638008 BioProcess=mitotic chromosome condensation*|MolFunction=DNA-directed DNA polymerase|CellComponent=nucleus

634049 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated

635953 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

633691 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638571 BioProcess=arsenite transport|MolFunction=arsenite transporter|CellComponent=integral plasma membrane protein

634387 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

636849 BioProcess=biological_process unknown|MolFunction=adenosinetriphosphatase|CellComponent=cellular_component unknown

634828 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

637993 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated

636903 BioProcess=meiosis|MolFunction=phospholipase|CellComponent=nucleus

637532 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638558 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638282 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

635344 BioProcess=mating (sensu *Saccharomyces*)|MolFunction=molecular_function unknown|CellComponent=plasma membrane

633336 BioProcess=not yet annotated|MolFunction=cytochrome c peroxidase|CellComponent=mitochondrion

633415 BioProcess=stress response|MolFunction=aldehyde dehydrogenase|CellComponent=cytoplasm

639267 BioProcess=protein amino acid geranylgeranylation|MolFunction=RAB-protein geranylgeranyltransferase|CellComponent=RAB-protein geranylgeranyltransferase

637227 BioProcess=iron homeostasis|MolFunction=ATP-binding cassette (ABC) transporter|CellComponent=mitochondrial inner membrane

634369 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636538 BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit
636512 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638141 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
634243 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm
633793 BioProcess=vesicle-mediated transport|MolFunction=molecular_function unknown|CellComponent=Golgi apparatus*
634808 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635272 BioProcess=rRNA-nucleus export*|MolFunction=not yet annotated|CellComponent=not yet annotated
636100 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635311 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm
636148 BioProcess=vacuolar acidification|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=vacuolar membrane (sensu Fungi)*
634389 BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)
637287 BioProcess=protein amino acid acetylation|MolFunction=peptide alpha-N-acetyltransferase|CellComponent=not yet annotated
633945 BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated
635634 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638427 BioProcess=chromatin modification|MolFunction=molecular_function unknown|CellComponent=nucleus
633912 BioProcess=vesicle-mediated transport|MolFunction=molecular_function unknown|CellComponent=cytoplasmic vesicle*
637718 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638680 BioProcess=pantothenate biosynthesis|MolFunction=molecular_function unknown|CellComponent=cytoplasm
633834 BioProcess=cell cycle|MolFunction=not yet annotated|CellComponent=not yet annotated
636041 BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated
635349 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639112 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639281 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636872 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636263 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637471 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637879 BioProcess=O-linked glycosylation*|MolFunction=alpha-1,2-mannosyltransferase|CellComponent=Golgi apparatus
636225 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636979 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
633372 BioProcess=ergosterol biosynthesis|MolFunction=C-14 sterol reductase|CellComponent=endoplasmic reticulum
638891 BioProcess=not yet annotated|MolFunction=glutamate dehydrogenase|CellComponent=not yet annotated
637346 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
634100 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638611 BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylserine decarboxylase|CellComponent=mitochondrion
636665 BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated
634414 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634151 BioProcess=ergosterol biosynthesis|MolFunction=lanosterol synthase|CellComponent=endoplasmic reticulum*

635625 BioProcess=establishment of cell polarity (sensu *Saccharomyces*)*|MolFunction=signal transducer*|CellComponent=bud tip

637302 BioProcess=di-, tri-valent inorganic cation transport|MolFunction=di-, tri-valent inorganic cation transporter|CellComponent=plasma membrane

633936 BioProcess=steroid biosynthesis|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638438 BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated

633363 BioProcess=vesicle-mediated transport|MolFunction=structural molecule|CellComponent=clathrin vesicle coat

637598 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm

636549 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

635142 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634168 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638385 BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated

970773 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown

639061 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

638615 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

634029 BioProcess=mRNA-nucleus export*|MolFunction=structural molecule|CellComponent=nuclear pore

970838 BioProcess=regulation of transcription, mating-type specific|MolFunction=transcription co-repressor|CellComponent=nucleus

638893 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

635822 BioProcess=response to osmotic stress*|MolFunction=actin monomer binding|CellComponent=actin cap (sensu *Saccharomyces*)*

634824 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

636202 BioProcess=not yet annotated|MolFunction=fattypolyglutamate synthase|CellComponent=not yet annotated

637284 BioProcess=pseudohyphal growth*|MolFunction=1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase|CellComponent=cellular_component un

639138 BioProcess=response to osmotic stress*|MolFunction=glycerol-1-phosphatase|CellComponent=cellular_component unknown

637812 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

636109 BioProcess=proline biosynthesis|MolFunction=glutamate-5-semialdehyde dehydrogenase|CellComponent=cytoplasm

637094 BioProcess=lactate metabolism|MolFunction=D-lactate dehydrogenase (cytochrome)|CellComponent=cytoplasm*

635994 BioProcess=not yet annotated|MolFunction=acylglycerone-phosphate reductase|CellComponent=not yet annotated

633531 BioProcess=establishment of cell polarity (sensu *Saccharomyces*)*|MolFunction=signal transducer*|CellComponent=intracellular

633490 BioProcess=sterol metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated

970752 BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated

637246 BioProcess=not yet annotated|MolFunction=transketolase|CellComponent=not yet annotated

636637 BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated

637411 BioProcess=tRNA processing|MolFunction=not yet annotated|CellComponent=not yet annotated

633421 BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)

638887 BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylserine decarboxylase|CellComponent=not yet annotated

635396 BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated

634232 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated

638799 BioProcess=polyamine transport|MolFunction=spermine transporter|CellComponent=vacuolar membrane

635428 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638460 BioProcess=not yet annotated|MolFunction=branched-chain amino acid aminotransferase|CellComponent=not yet annotated
636702 BioProcess=protein folding*|MolFunction=protein disulfide isomerase|CellComponent=not yet annotated
639520 BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=nucleus
634970 BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=hydrogen-transporting .
634073 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636371 BioProcess=not yet annotated|MolFunction=AMP deaminase|CellComponent=not yet annotated
634464 BioProcess=not yet annotated|MolFunction=orotate phosphoribosyltransferase|CellComponent=not yet annotated
635234 BioProcess=methionine metabolism|MolFunction=methionine adenosyltransferase|CellComponent=cytoplasm
637392 BioProcess=stress response*|MolFunction=alpha,alpha-trehalose-phosphate synthase (UDP-forming)|CellComponent=alpha, alpha-trehalose-phosph
638414 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639274 BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=mitochondrion*
637380 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636922 BioProcess=basic amino acid transport|MolFunction=basic amino acid transporter|CellComponent=plasma membrane
635951 BioProcess=SRP-dependent, co-translational membrane targeting, translocation|MolFunction=transporter|CellComponent=translocon
638929 BioProcess=nucleotide-excision repair, DNA incision, 5 to lesion|MolFunction=single-stranded DNA specific endodeoxyribonuclease|CellComponent=
637927 BioProcess=not yet annotated|MolFunction=glycine hydroxymethyltransferase|CellComponent=not yet annotated
638406 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
639349 BioProcess=gluconeogenesis*|MolFunction=fructose-bisphosphate aldolase|CellComponent=cytoplasm*
633922 BioProcess=not yet annotated|MolFunction=acylglycerone-phosphate reductase|CellComponent=not yet annotated
635607 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638655 BioProcess=cytoskeleton organization and biogenesis*|MolFunction=cytoskeletal protein binding*|CellComponent=actin cortical patch (sensu Saccha
635366 BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
638127 BioProcess=Golgi to vacuole transport|MolFunction=molecular_function unknown|CellComponent=AP-3 adaptor complex
635210 BioProcess=branched chain family amino acid biosynthesis|MolFunction=ketol-acid reductoisomerase|CellComponent=mitochondrion
636984 BioProcess=not yet annotated|MolFunction=phosphoserine aminotransferase|CellComponent=not yet annotated
635119 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636124 BioProcess=low affinity iron transport|MolFunction=iron transporter|CellComponent=integral plasma membrane protein
638587 BioProcess=glycolysis*|MolFunction=pyruvate kinase|CellComponent=cytosol
638961 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636308 BioProcess=histidine biosynthesis|MolFunction=histidinol dehydrogenase*|CellComponent=cell
634537 BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638090 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
638442 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635434 BioProcess=leucine biosynthesis|MolFunction=2-isopropylmalate synthase|CellComponent=cytoplasm*
638876 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635071 BioProcess=branched chain family amino acid biosynthesis|MolFunction=acetolactate synthase|CellComponent=mitochondrion

635493 BioProcess=signal transduction|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
639037 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636681 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
637816 BioProcess=hexadecanal biosynthesis|MolFunction=3-oxoacyl-[acyl-carrier protein] synthase|CellComponent=mitochondrion
638523 BioProcess=intracellular accumulation of glycerol|MolFunction=glycerol-3-phosphate dehydrogenase (NAD+)|CellComponent=cytoplasm
633891 BioProcess=tricarboxylic acid cycle*|MolFunction=isocitrate dehydrogenase (NAD+)|CellComponent=mitochondrion*
636855 BioProcess=acetate metabolism*|MolFunction=acetyl-CoA hydrolase|CellComponent=cytoplasm
635307 BioProcess=tricarboxylic acid cycle*|MolFunction=fumarate hydratase|CellComponent=cytosol*
638564 BioProcess=sphingolipid metabolism*|MolFunction=sphingosine-1-phosphate phosphatase|CellComponent=endoplasmic reticulum
635672 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635992 BioProcess=not yet annotated|MolFunction=transaldolase|CellComponent=not yet annotated
635261 BioProcess=G1/S transition of mitotic cell cycle*|MolFunction=cyclin-dependent protein kinase, regulator|CellComponent=cellular_component unkno
639298 BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
636889 BioProcess=not yet annotated|MolFunction=carboxypeptidase C|CellComponent=cytoplasm*
635215 BioProcess=mitochondrial translocation|MolFunction=protein transporter|CellComponent=mitochondrion*
637131 BioProcess=tRNA splicing|MolFunction=molecular_function unknown|CellComponent=not yet annotated
635415 BioProcess=amino acid metabolism*|MolFunction=malate dehydrogenase (oxaloacetate decarboxylating)|CellComponent=mitochondrion

omplex*

component=not yet annotated

yltransferase comple

knowr

ATP synthase, stator stalk (sensu Eukarya)

hate synthase complex (UDP-forming)

=nucleotide excision repair factor 1

zromyces)

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